

Fig. 1

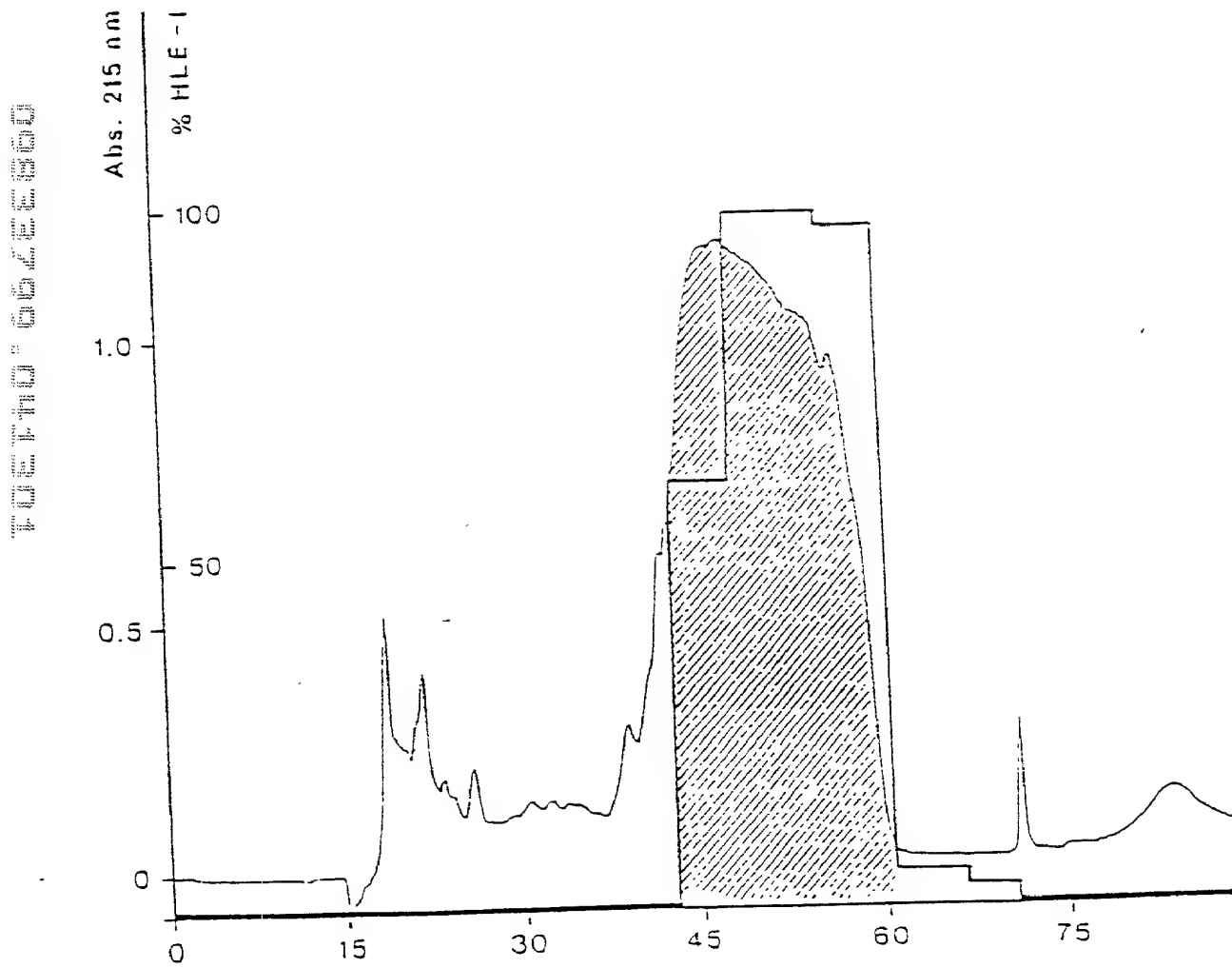


Fig. 2

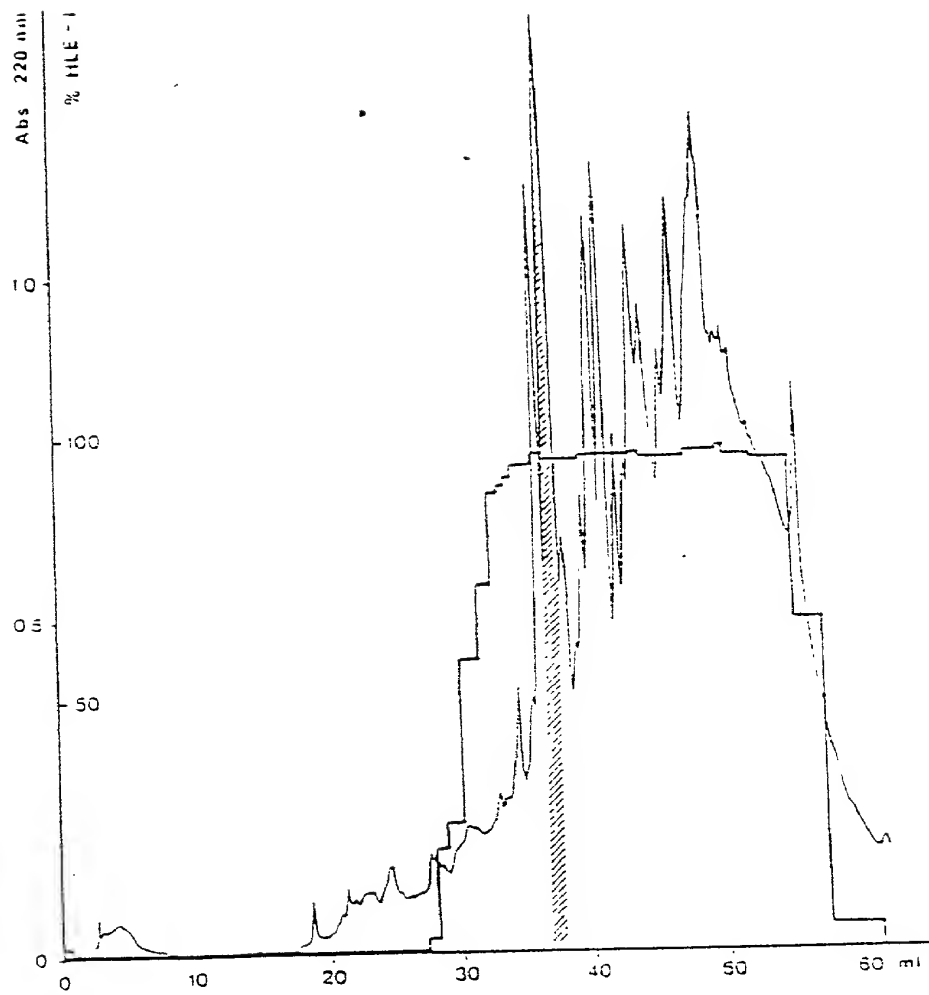


Fig. 3



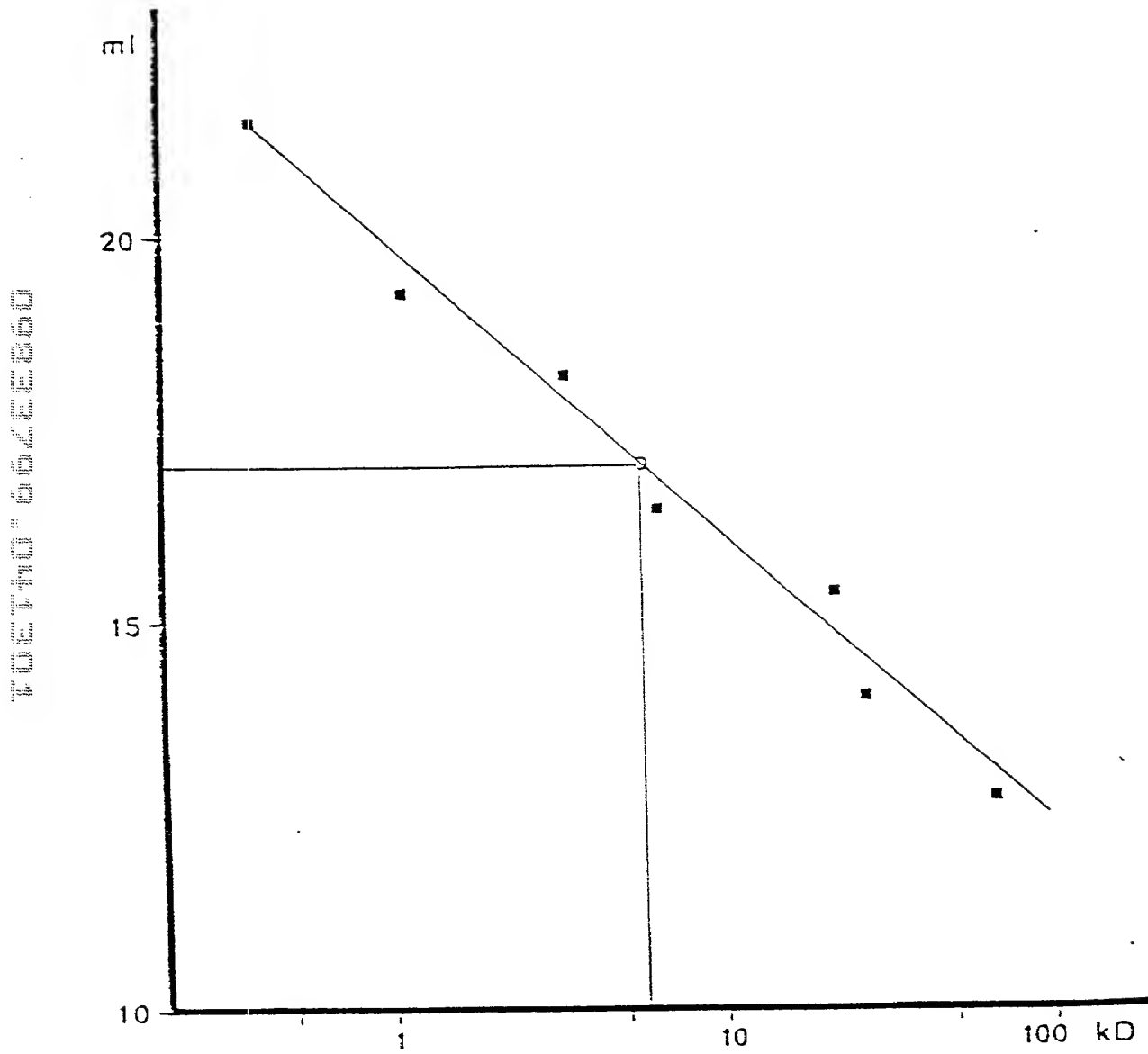


Fig. 5

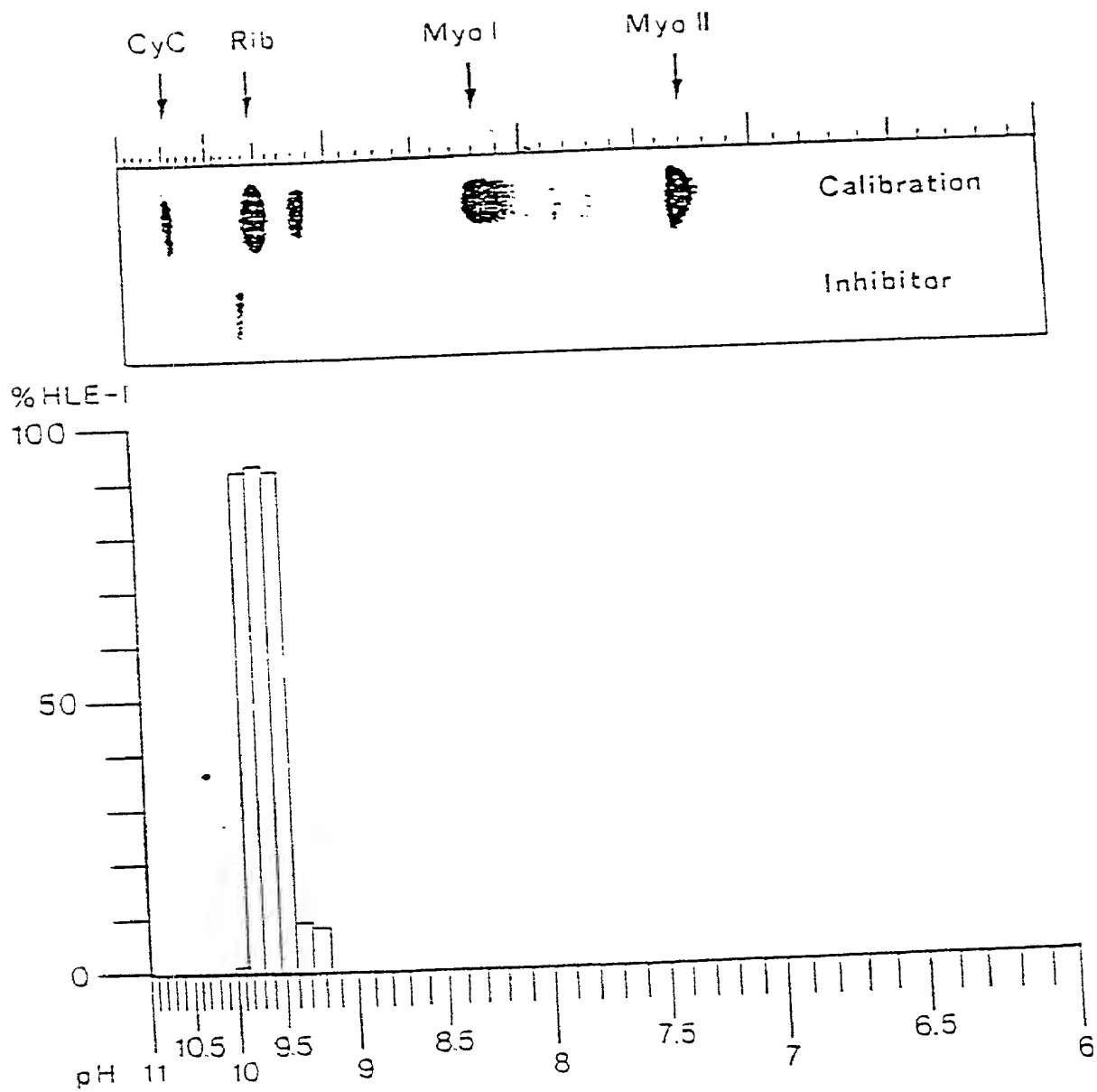


Fig. 6

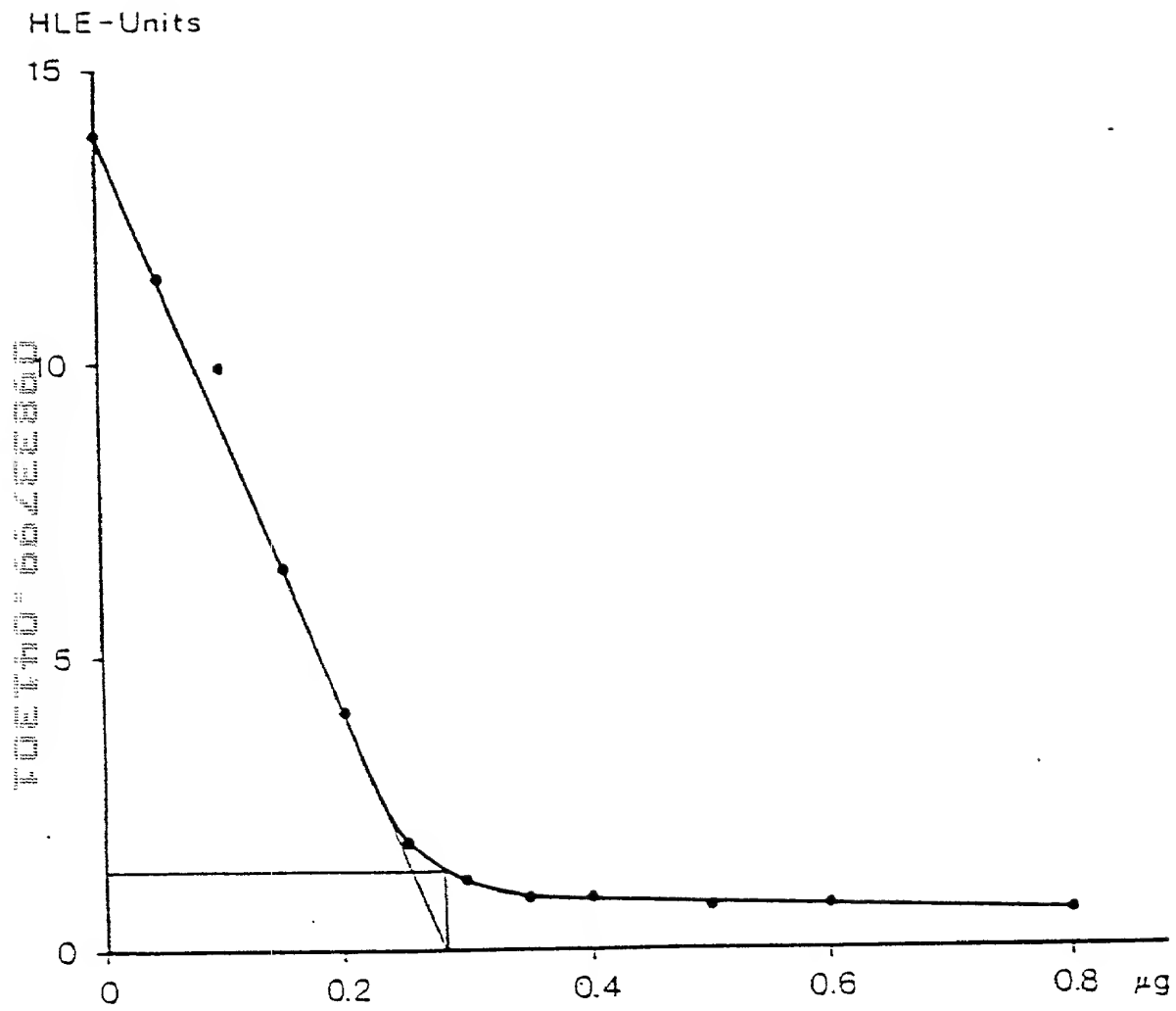
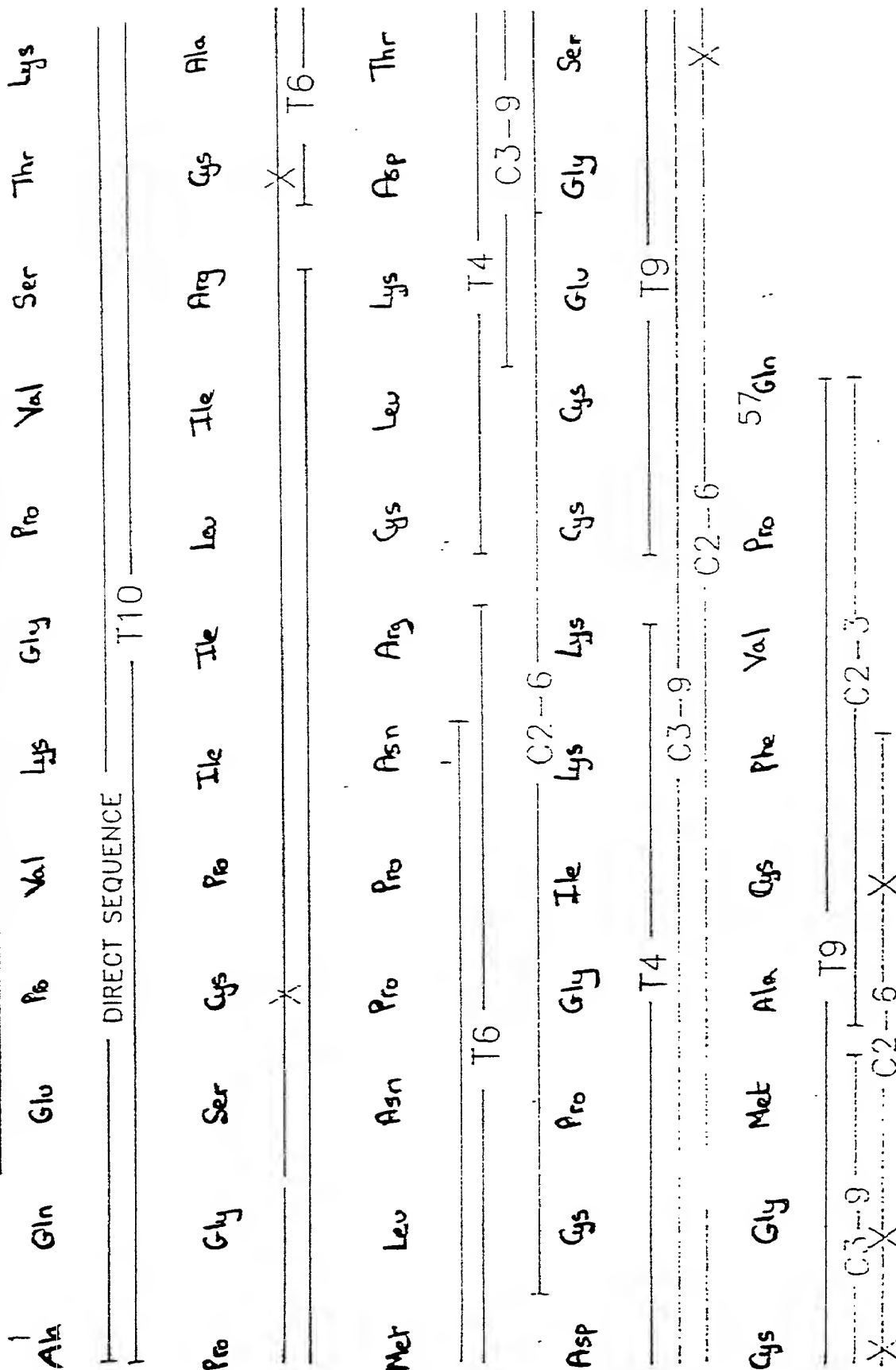


Fig. 7

PROTEIN SEQUENCE OF ELASTASE INHIBITOR



X=UNIDENTIFIED T=TRYPTIC FRAGMENTS C=CHYMOTRYPTIC FRAGMENTS

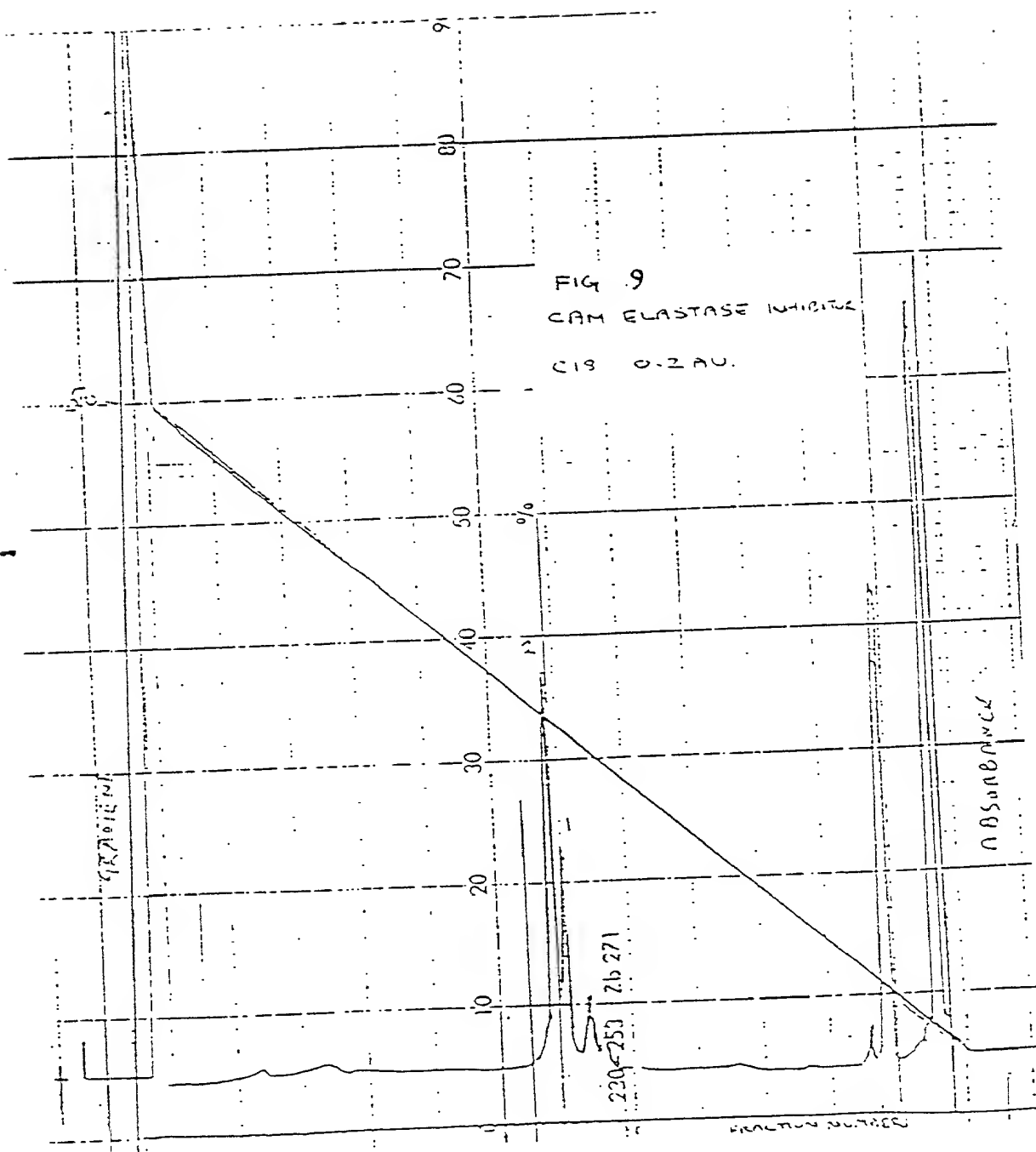
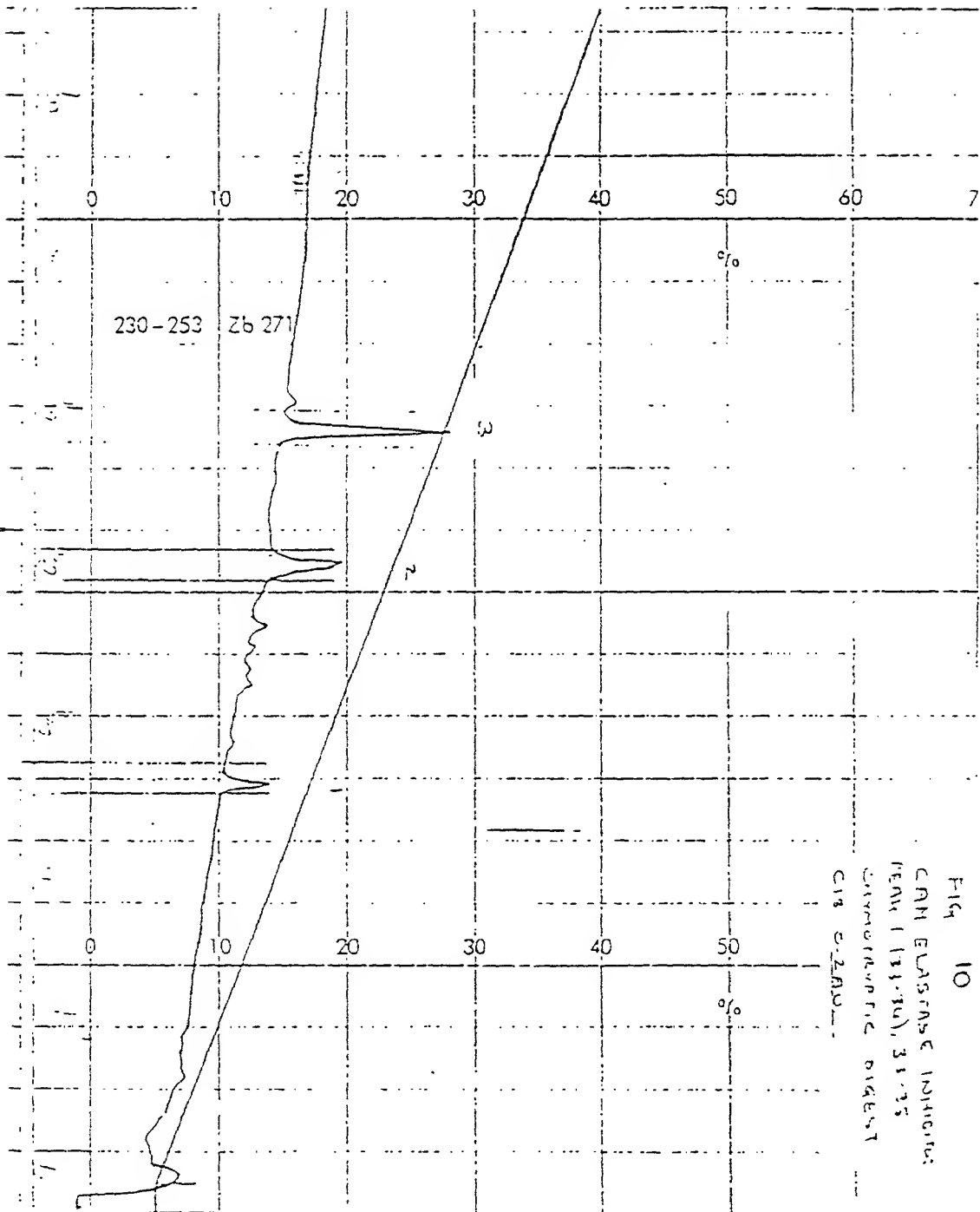


FIG 9



0083799-041304

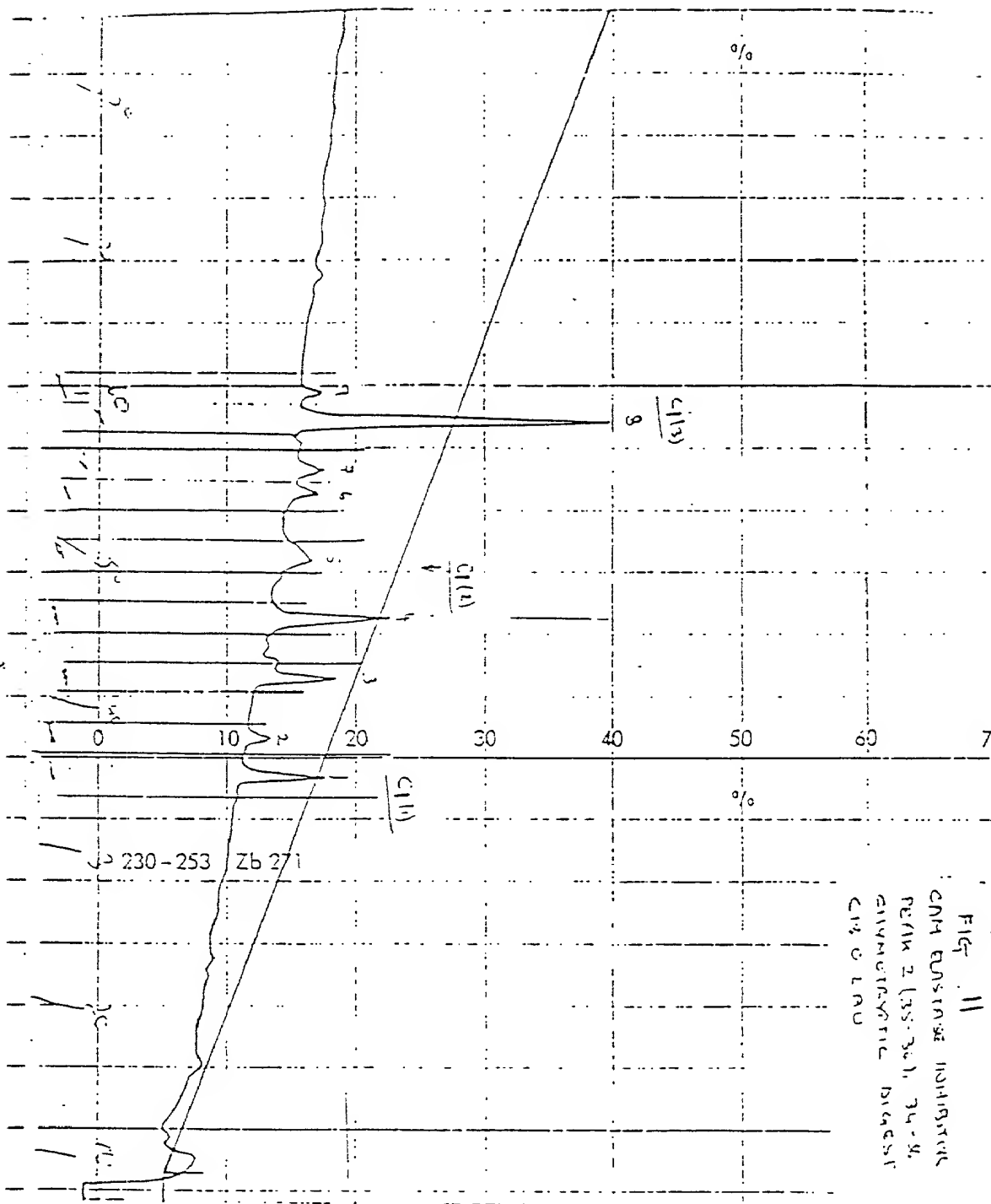


FIG. 11  
 CATHODOLUMINESCENCE SPECTRUM  
 OF PZT (35-30), 34-38,  
 ANTIMONY DOPED  
 CATHODOLUM

FIG 11

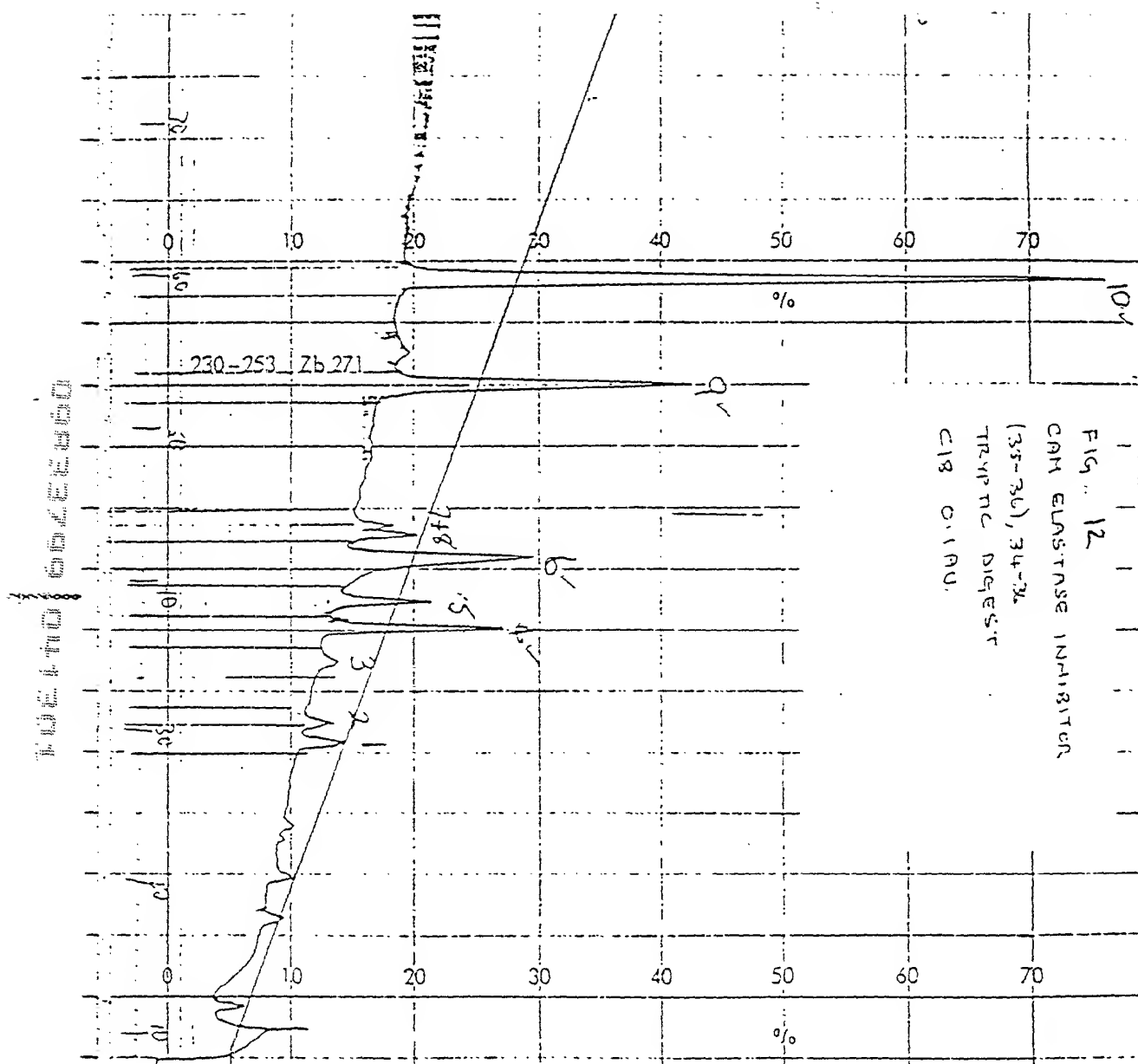
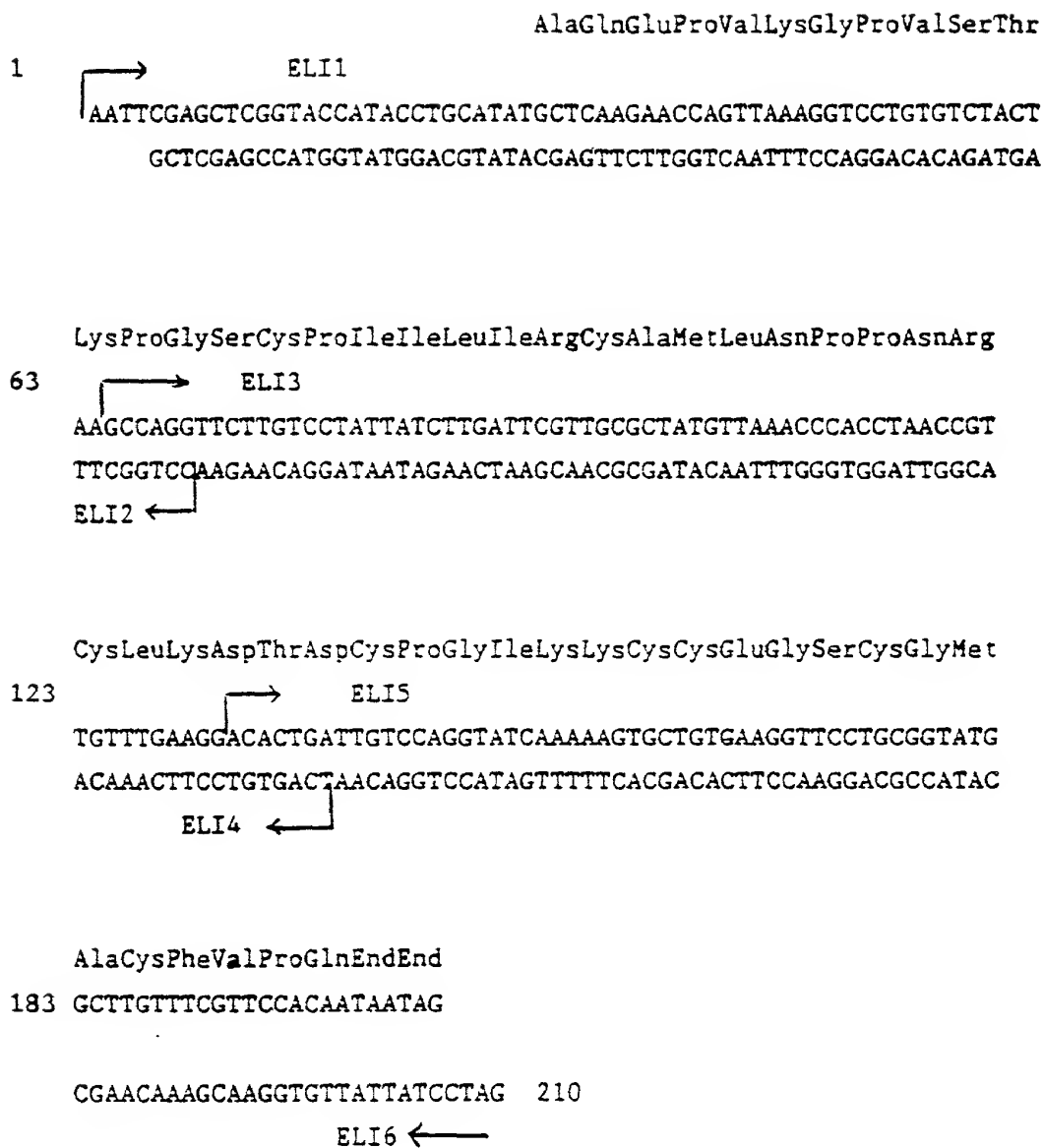


FIG. 12  
CAN ELASTASE INHIBITOR  
(35-36), 34-36  
TRYPTIC DIGEST  
CIR 0.1100

FIG 12

Figure 13

P = A or G

Ala Gln Glu Pro Val Lys Gly Pro Val Ser Thr Lys Pro Gly Ser Cys  
GCG CAA GAG CCA GTC AAA GGT CCA GTC TCC ACT AAG CCT GGC TCC TGC  
5' DNA  
Sequence

Leu Lys Asp Thr Asp Cys Pro Gly Ile Lys Lys Cys Cys Glu Gly Ser

Cys Gly Met Ala Cys Phe Val Pro Gln  
TGC GGG ATG GCC TGT TTC GTT CCC CAG TAG GAGGGAGCCGGTCCTTGCTGCACCTGT

Poly A 3'  
signal

Z = T, C or A  
P = A or G

FIGURE 16

10 30 50  
 . . . . .  
GGAATTCCGGTTCTCATCGCTGGGACGCTGGTTCTAGAGGCAGCTGTCACGGGAGTTCC  
 EcoRI XbaI  
 F L I A G T L V L E A A V T G V P  
 |-----IN-FRAME UPSTREAM PROTEIN SEQUENCE-----  
 70 90 110  
 . . . . .  
 TGTAAAGGTCAAGACACTGTCAAAGGCCGTGTTCCATTCAATGGACAAGATCCCGTTAA  
 V K G Q D T V K G R V P F N G Q D P V K  
 130 150 170  
 . . . . .  
 AGGACAAGTTTCAGTTAAAGGTCAAGATAAAGTCAAAGCGCAAGAGCCAGTCAAAGGTCC  
 G Q V S V K G Q D K V K  
 AlaGlnGluProValLysGlyPr  
 |--ELASTASE INHIBITOR--

Cont'd 16b of 19

16a of 19  
 16b of 19  
 16c of 19  
 16d of 19  
 16e of 19  
 16f of 19  
 16g of 19  
 16h of 19  
 16i of 19  
 16j of 19  
 16k of 19  
 16l of 19  
 16m of 19  
 16n of 19  
 16o of 19  
 16p of 19  
 16q of 19  
 16r of 19  
 16s of 19  
 16t of 19  
 16u of 19  
 16v of 19  
 16w of 19  
 16x of 19  
 16y of 19  
 16z of 19

## FIGURE 16 CONTINUED

190 210 230  
 AGTCTCCACTAAGCCTGGCTCCTGCCCCATTATCTTGATCCGGTGCGCCATGTTGAATCC  
 oValSerThrLysProGlySerCysProIleIleLeuIleArgCysAlaMetLeuAsnPr

250 270 290  
 CCCTAACCGCTGCTTGAAAGATACTGACTGCCCAGGAATCAAGAAGTGCTGTGAAGGCTC  
 oProAsnArgCysLeuLysAspThrAspCysProGlyIleLysLysCysCysGluGlySe

310 330 350  
 TTGCGGGATGGCCTGTTTCGTTCCCCAGTGAGAGGGAGCCGGTCCTTGCTGCACCTGTGC  
 rCysGlyMetAlaCysPheValProGlnEnd

370 390 410  
 CGTCCCAGAGCTACAGGCCCATCTGGTCCTAAGTCCCTGCTGCCCTTCCCCTTCCCAC

430 450 470  
 ACTGTCCATTCTTCCTCCCATTTCAGGATGCCACGGCTGGAGCTGCCTCTCTCATCCACT

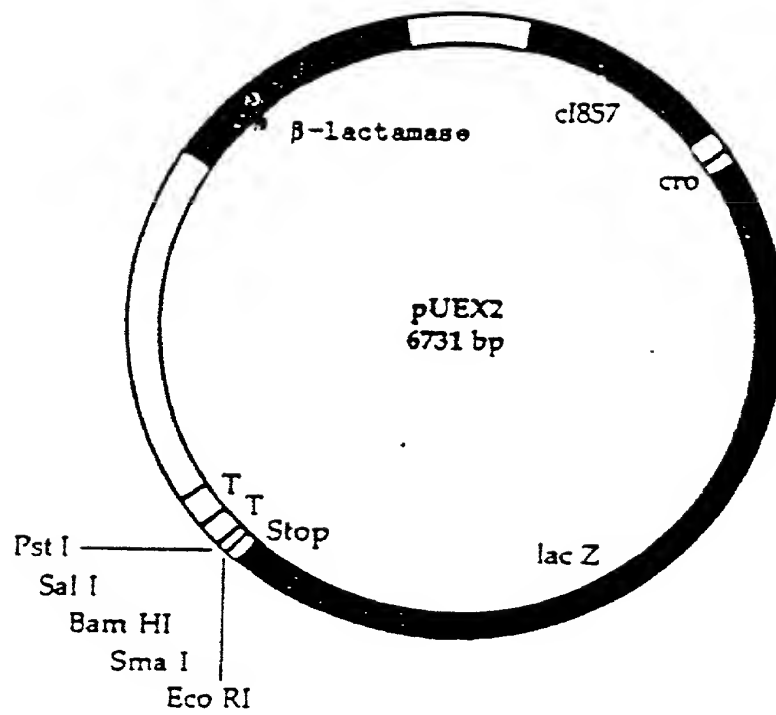
490  
 TTCCAATAAAAGAGTTCCGGAATTC

Poly A

EcoRI

signal

FIGURE 16 CONTINUED



EcoRI   SmaI   BamHI   SalI   PstI  
 |   |   |   |   |  
 pUEX2   GAA   TTC   CCG   GGG   ATC   CGT   CGA   CCT   GCA   GCC   AAG   CTT   GCT   GAT   TGA  
 Glu   Phe   Pro   Gly   Ile   Arg   Arg   Pro   Ala   Ala   Lys   Leu   Ala   Asp   \*\*\*

FIG 17

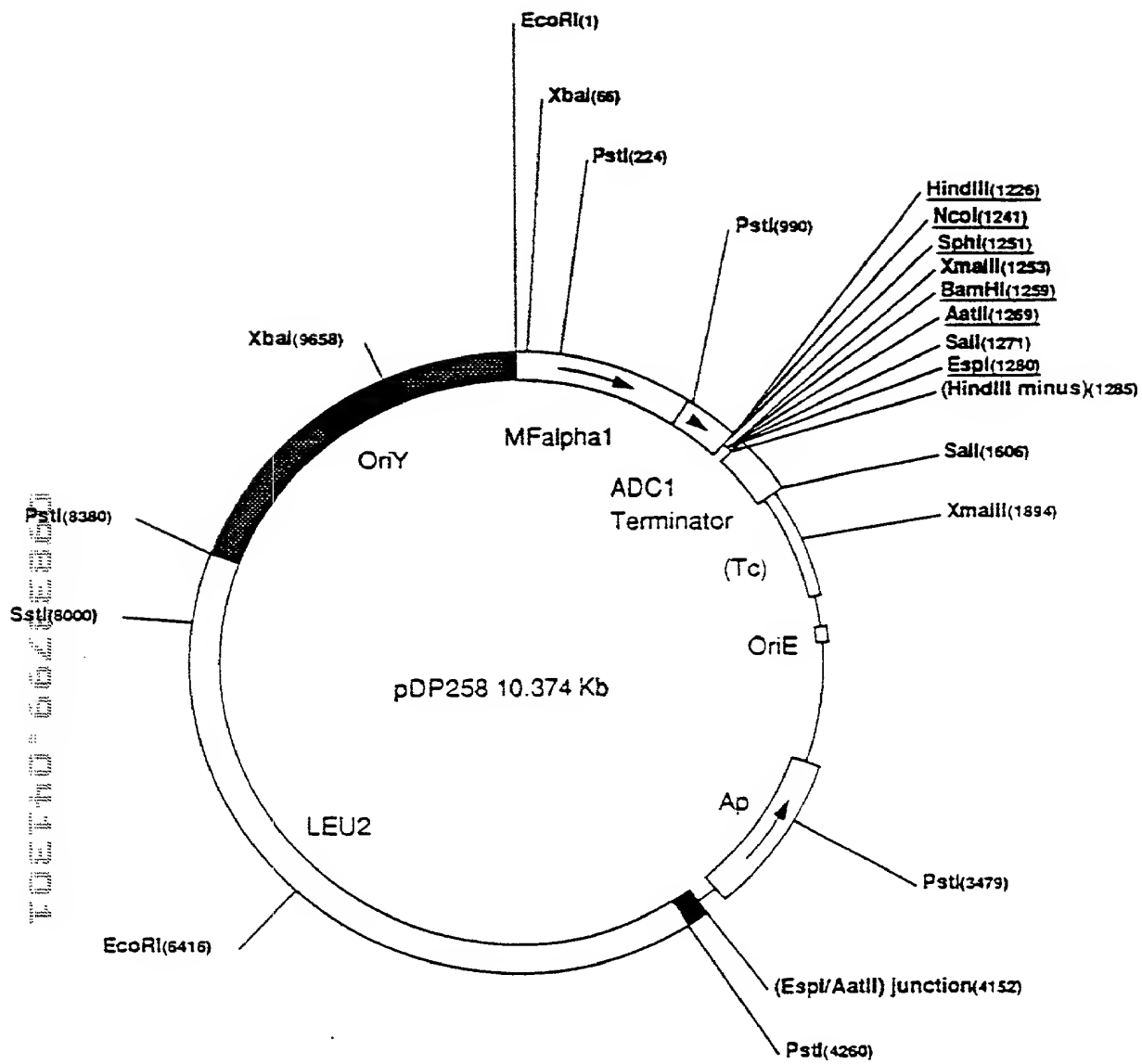


FIG 18

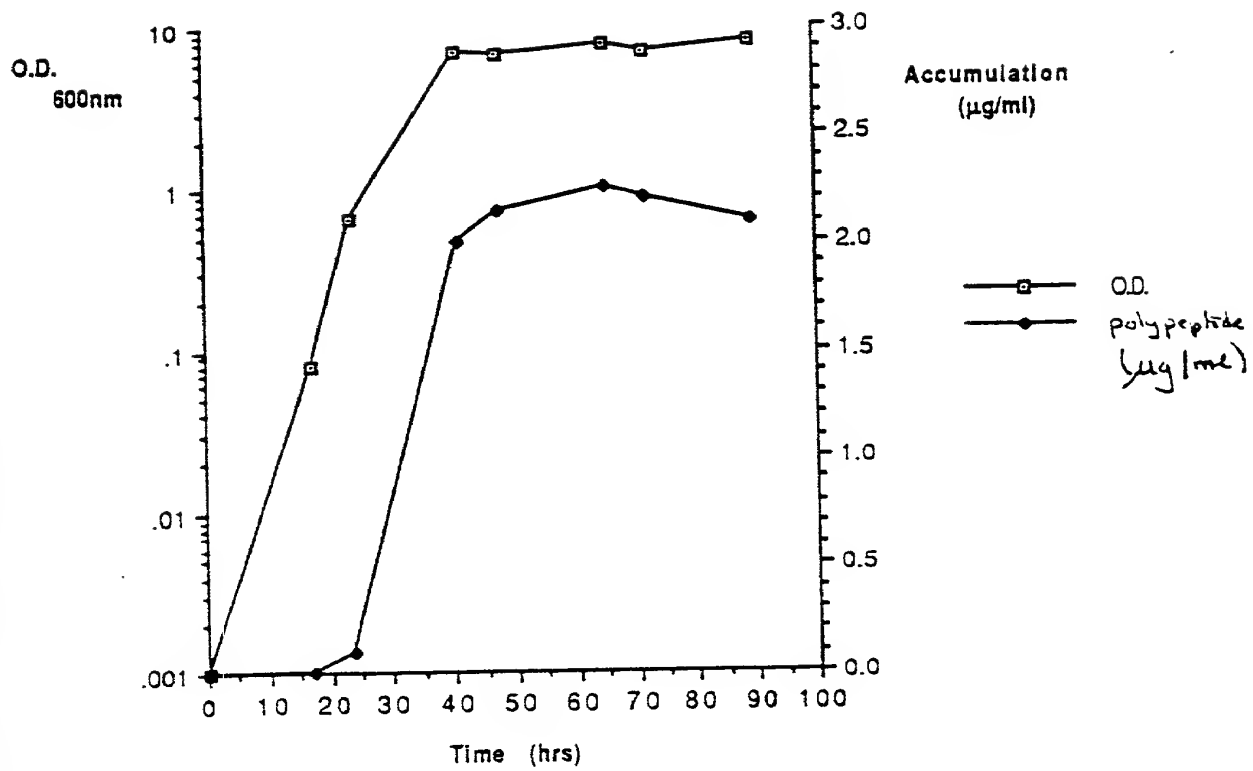


FIG 19